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Growth performance, pork quality, and excretion characteristics of pigs fed Bt corn or non-genetically modified corn at two slaughter weights

Maareen Gesmundo Custodio
Iowa State University

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Maareen Gesmundo Custodio

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Wendy J. Powers, Major Professor
Elisabeth Huff-Lonergan
Mark S. Honeyman
Kenneth J. Prusa

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Iowa State University

This is to certify that the master's thesis of

Maareen Gesmundo Custodio

has met the thesis requirements of Iowa State University

Signatures have been redacted for privacy

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CHAPTER 1. INTRODUCTION

Recent advances in biotechnology have brought enormous changes in agriculture. These changes are driven by the need to supply food for the ever-increasing world population. One of these changes is the introduction of novel genes into crops to improve yield and/ or quality. This approach has resulted in the production of "genetically modified" crops that possess the ability to tolerate pests and herbicides. Crop growers have rapidly adopted the use of biotechnology-derived seeds since its approval in the 1990s, because of the potential benefits in terms of improvement in agronomic traits and savings due to less usage of herbicides and pesticides.

One such crop that has been developed by genetic engineering is Bt corn. Bt corn was produced by incorporating a gene from a naturally-occurring bacterium, *Bacillus thuringiensis (Bt)*. This organism expresses a gene that encodes for crystal-like proteins that kill a specific group of insects. For many years, the practice of spraying Bt as a biopesticide in corn fields was conducted as a means of controlling an economically important pest, the European corn borer (*Ostrinia nubilalis*). However, this practice required repeated application and necessitated the use of insecticides. To overcome these disadvantages, plant scientists inserted the *Bt* gene directly into corn DNA.

The National Agricultural Statistics Service reported in 2003 that 40% of the corn planted in the United States was biotechnology-derived, of which 25% was of the Bt variety, 11% was herbicide-resistant, and 4% was both herbicide and insect-resistant. The increasing cultivation of genetically modified corn is of interest to livestock producers. Diets of farm animals consist largely of plant-derived food such as corn. Genetic modification of corn raises questions of whether the nutritive value of the crop is unintentionally altered, and

hence, might potentially affect the growth and performance of food animals in a negative manner.

In grower-finisher pigs, corn is a major constituent of the diet. It is of interest, therefore, to investigate whether the inserted gene influences the growth performance and carcass quality of pigs fed Bt corn, and the excretion of nutrients such as nitrogen and phosphorus. Feeding trials are necessary to demonstrate the safety of genetically modified feeds with regard to performance of animals and the quality of foods of animal origin. The objective of this study was to compare the growth performance, carcass, and excretion characteristics of pigs fed diets containing either Bt event 11 corn, or combined corn from non-genetically modified inbred lines.

Thesis organization

This thesis is organized into six chapters including a general introduction, review of literature, materials and methods, results, discussion and general conclusions.

CHAPTER 2. LITERATURE REVIEW

The Concept of Genetic Modification

The terms "genetically modified", "genetically engineered", "transgenic", and "recombinant" are all used to describe living organisms, such as plant, animals or microorganisms, which carries DNA introduced into them by means other than the combination of a sperm and an egg (Roller and Harlander, 1998). Manipulation of genetic traits of plants and animals is not a new concept, but rather a practice that has been conducted by man for centuries through selective breeding based upon the inherent characteristics of the organism (Pfeiffer, 2003). Genetic engineering involves the use of recombinant DNA technology, in which a DNA molecule is altered by inserting into it a segment of foreign DNA. (Alcamo, 2001).

Traditional breeding methods differ from modern recombinant DNA technology in several ways. First, the random nature of classical breeding is reduced by using recombinant DNA technology. DNA can be directly manipulated to achieve a desired trait. Secondly, the use of modern DNA techniques gives desired results in a much quicker and more predictable manner. On the other hand, classic Mendelian genetics requires generations to achieve observable changes. Finally, it is possible to cross the species barrier using modern recombinant DNA technologies, something that cannot be achieved using traditional breeding methods (Roller and Harlander, 1998).

Global Adoption of Genetically Modified Crops

Genetically modified (GM) crops that resist insect pests or can tolerate herbicides have been rapidly adopted by more than a dozen countries since they were approved for usage in 1996 (Figure 1). In 2003, the area of land planted worldwide with biotech crops

increased from 145 to 167.3 million acres (International Service for Acqusition of Agri-biotech Applications, 2003).

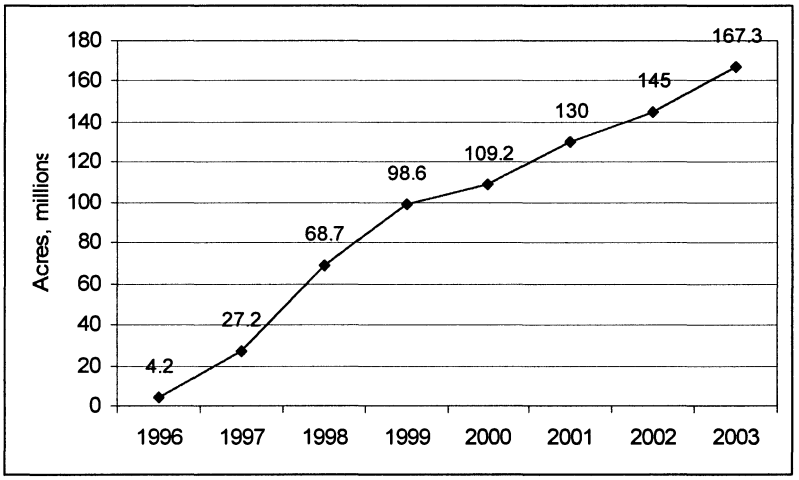

Figure 1. Global area of GM crops.
Source: International Service for the Acquisition of Agri-biotech Applications (ISAAA)

The leading growers of biotech crops are the United States, Argentina, Canada, China, and more recently, Brazil and South Africa (Chrispeels and Sadava, 2003; ISAAA, 2003). It was estimated that 7 million farmers in 18 countries now plant biotech crops (ISAAA, 2003). However, despite the rapid adoption of GM crops in many parts of the world, this technology has aroused some anxiety in the general public (Straughan, 1998). Genetically engineered crops have been banned in some parts of Western Europe and in few localities in the U.S. (Chrispeels and Sadava, 2003).

At present, the major GM crops are soybean, maize, cotton, and canola. The ISAAA (2003) reported that herbicide resistance is the most dominant trait (75%) among GM crops in 2002, followed by insect resistance (17%), and the combination of herbicide tolerance and insect resistance (8%).

The United States is the largest grower of GM crops, producing 68% of the world's total (ISAAA, 2003). In the U.S., GM crop acreage grew 10% in 2003, primarily from

growth in planting of Bt corn and biotech soybeans (Figure 2). Planting of GM soybean increased from 75% to 81% in 2003, while GM corn increased from 34% to 40% (NASS, 2004).

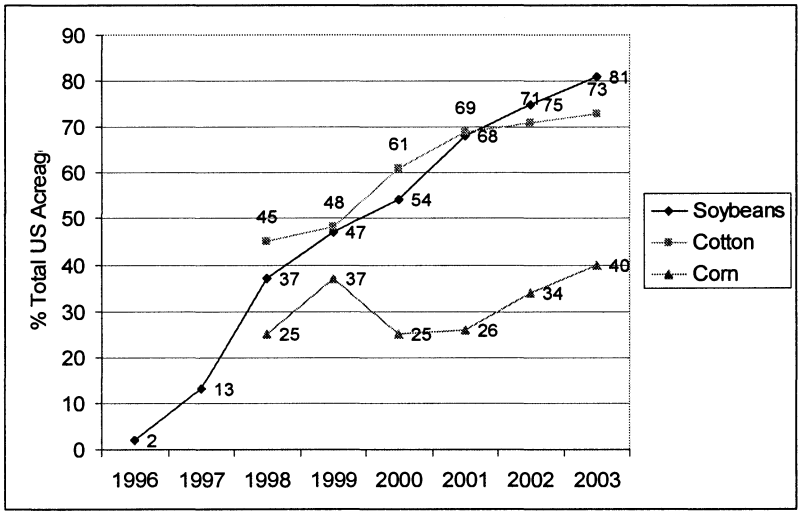

Figure 2. U.S. acreage (%) planted with GM crops.
Source: National Agricultural Statistics Service (NASS)

Genetically Modified Crops Used Commonly as Animal Feeds

Transgenic crops that are commonly used as source of livestock feed components include corn, soybean, canola, cottonseed, and potato (Agbios, 2003). These crops are usually modified to express the trait for insect resistance, herbicide resistance, or combination of both. In the case of potato, the gene for virus resistance was incorporated into its DNA. Table 1 shows a summary of the traits expressed and associated genes that have been incorporated into crops commonly used as animal feeds.

Table 1. Traits expressed and associated genes that have been incorporated into crops used commonly as animal feeds and have been commercialized.

Trait	Genetic element(s)	Gene Source
Insect resistance	Cry1Ab, Cry1Ac, Cry9C, Cry3A, Cry1F	*Bacillus thuringiensis*
Glufosinate herbicide tolerance	Phosphinothricin N-acetyltransferase	*Streptomyces hygroscopicus* or *viridochromogenes*
Glyphosate herbicide tolerance	5-enolpyruvylshikimate-3-phosphate synthase (EPSPS)	*Agrobacterium tumefasciens* strain CP4; or modified endogenous maize enzyme
Male sterility	Bamase ribonuclease	*Bacillus amyloliquifasciens*
Sulfonyl urea herbicide tolerance	Variant form of acetolactate synthase	*Nicotiana tabacum* (tobacco)
Oxynil herbicide tolerance	Nitrilase	*Klebsiella pneumonia* subsp. *ozanae*
Modified seed fatty acid profile	Delta –12 desaturase	*Glycine max* (soybean); coordinate suppression of endogenous gene
Virus resistance	Coat protein Helicase/ replicase	potato virus Y potato leafroll virus

Source: AGBIOS, 2003

Insect resistance. Insect resistance in GM crops is made possible by the insertion of the gene from a bacterium that encodes for proteins that kill specific group of insects. *Bacillus thuringiensis* is a gram positive, rod-shaped spore-forming bacterium which naturally occurs in soil (Glare and O'Callaghan, 2000). Its use as an insecticide is due to its capability of producing toxins which kills specific group of insects. The endotoxins, also known as the crystal-like proteins (Cry toxins), are found in the majority of *Bacillus thuringiensis* strains and is produced during sporulation. The practice of spraying Bt in crops has been considered a safe method of controlling the European corn borer (*Ostrinia nubilalis*), an economically devastating pest (Benedict, 2003). Endotoxins, when ingested at

high doses by these insects, will bind to receptor sites in the cells of the gut epithelium. This will lead to perforations in the membrane, which eventually result in the disruption of ion exchange between epithelial cells and the gut lumen. The breakdown of the ion transport system ultimately leads to death of the insect (Glare and O'Callaghan, 2000). At lesser doses, ingestion of endotoxins will result in the reduction of pH in the gut lumen, allowing the spores to germinate. Thus, there is rapid multiplication of the organism that will lead to septicemia, and eventually death of the insect (Glare and O'Callaghan,2000).

The *Bt* genes (Cry genes) were the first available genes for genetic engineering of crops for pest resistance. Crops with the *Bt* gene were developed as an alternative to spraying with insecticide. The first crops with inserted *Bt* genes were planted in 1996 and this included corn, cotton and potatoes (Chrispeels and Sadava, 2003).

Herbicide resistance. Herbicide resistant/ tolerant crops carry the genes that make them resistant to herbicides that are normally lethal or highly damaging to the plants. The most common herbicide tolerance is towards glyphosate and glufosinate. An enzyme called 5-enolpyruvlyshikimate-3-phosphate synthase (EPSPS) is naturally present in plants and plays a role in the synthesis of aromatic amino acids; phenylalanine, tyrosine, tryptophan (Tranel, 2003). Glyphosate, an amino acid analogue, selectively inhibits the activity of EPSPS enzyme and interferes with the synthesis of aromatic amino acids. Shutting off the synthesis of these amino acids in plants affects normal growth and maintenance and will result in death of the plant. Thus, when herbicide with the active ingredient glyphosate is sprayed in corn fields, the corn plant itself will be at risk of being destroyed. Because weeds are a serious problem in crop production, farmers must be provided with new alternatives of managing weed control. The source for the glyphosate resistance trait is the *Agrobacterium.*

The gene was inserted into selected crops, resulting in Roundup® Ready plants because they are resistant to the Roundup® herbicide which contains glyphosate as the active ingredient (Tranel, 2003).

Transgenic herbicide resistant crops that metabolize particular herbicides have also been developed and commercialized. These crops resist the action of glufosinate by metabolizing this compound. Glufosinate, also called phosphinothricin, is a synthetic version of a toxin produced by *Streptomyces hygroscopicus* or *S. viridochromogenes*. Glufosinate kills plants by inhibiting the production of glutamine, which results in the accumulation of ammonia. Glufosinate-resistant crops carry the *pat* gene which encodes for phophinothricin N-acetyltransferase (PAT), the enzyme that degrades glufosinate (Agbios, 2003).

Virus resistance. Potato is currently the only crop with viral resistance trait that is used as feed component for livestock (Faust, 2002). These crops were developed to resist the devastating effects of potato virus Y and potato leafroll virus. Genes that encode for viral coat proteins were introduced into the DNA of potato. Because the viral coat proteins are expressed naturally in potatoes which have been infected with the virus, no safety-related issues are expected for animals that consume crops with viral resistance trait (Faust and Glenn, 2002).

The Bt event 11. The Bt 11 corn variety was developed to be both insect-resistant and herbicide-tolerant. It was genetically engineered through the introduction of the *cry1Ab* gene from *Bacillus thuringiensis* and the *pat* gene from *Streptomyces viridochromogenes* (Agbios, 2003). Direct DNA transfer served as the method of introduction. The *cry1Ab* gene expresses the protein *cry1Ab*, a delta-endotoxin for the control of the European corn borer. The *pat* gene regulates the expression of phosphinothricin N-acetyltransferase (PAT), an enzyme that

metabolizes glufosinate (Agbios, 2003). The *cry1Ab* proteins have been shown to be expressed in leaf, root, pollen, and kernels of corn (U.S. EPA, 2000).

Feeding Genetically Modified Crops to Livestock

Swine. Research on the effect of feeding Bt corn on the performance of pigs has been limited. Weber et al. (2000) conducted a feeding trial on growing pigs and found that feeding diets containing Bt corn had no deleterious effects on growth performance. No differences were measured in average daily gain (ADG), average feed intake, or feed efficiency between pigs fed any of the three corn sources; Bt, non-Bt isogenic counterpart, or commodity-sourced corn. Pigs fed Bt and non-Bt corn did not differ in carcass weight, however, pigs fed commodity-sourced corn had significantly heavier carcass weights and greater dressing percentages. Percent lean, and 10^{th} rib backfat were lesser in pigs fed isogenic corn than in pigs fed Bt or commodity-sourced corn. Marbling scores were highest for pigs fed Bt and isogenic corn.

The absence of difference in growth performance was also observed by Reuter et al. (2002) in a study comparing diets containing genetically-modified Bt maize (NX6262) with its parental isoline. They concluded that diets containing Bt maize can be fed to growing-finishing pigs without significant impacts on feed consumption, daily weight gain, and energy efficiency. This study was preceded by a study which showed that the Bt and non-Bt varieties of corn fed had no significant difference in metabolizable energy (ME) values, nitrogen free extract (NFE), and protein digestibility (Aulrich et al., 2001).

Hyun et al. (2004) compared the growth performance and carcass characteristics of barrows and gilts fed either Roundup® Ready corn (NK603) or three other non-transgenic (conventional) corn lines. There were no significant corn effects observed for feed intake,

ADG, and gain to feed ratio. Sex differences were observed, with barrows having greater overall feed intake and ADG than gilts ($P < 0.05$). However, gilts had greater gain to feed ratio than barrows during the finisher stage ($P < 0.01$). Carcass characteristics showed no significant corn effects on measures obtained (backfat thickness; *longissimus* muscle area; hot carcass weight; ham, loin, and shoulder weights). Barrows had greater hot carcass, and shoulder weight than gilts. In addition, backfat thickness was greater in barrows than gilts ($P < 0.05$), but there were no differences in *longissimus* muscle area between sexes. Analyses of quality (marbling, firmness, pH, color) and chemical composition of the *longissimus* muscle revealed no differences between pigs fed Roundup® Ready corn and conventional corn.

Poultry. A study in broiler chickens showed no significant difference in body weight between groups fed transgenic (Bt Event 176) and non-transgenic corn but differences in feed conversion were observed (Brake and Vlachos, 1998). Birds that received diets comprised of transgenic corn exhibited improved adjusted feed conversion ratios at 28 and 38 d of age. In addition, birds offered the Bt corn diet exhibited a significant increase in breast and *pectoralis minor* yield. However, they were not able to attribute the observed differences to the presence of the *Bt* gene. In contrast with these results, Brake et al. (2003) found no corn source effects on carcass yield of birds fed with Bt Event 11.

Performance of broilers fed corn varieties with herbicide resistance (Roundup® Ready NK603) and combined insect protection and glyphosate tolerance (YieldGard MON 810 × Roundup® Ready NK603) was investigated by Taylor et al. (2003). They found similar feed conversion between groups fed GM corn and non-GM corn. Chill weights, thigh, drum and wing weights were not affected by diets. However, breast meat and fat pad weights were different across treatments. In a similar study using different corn varieties (YieldGard

MON 810, and YieldGard x Roundup® Ready GA21), the same investigators confirmed the results for the previous experiment with the exception of differences noted between breast weights across treatments.

All studies mentioned suggested that feeding genetically modified corn to poultry poses no detrimental effects in terms of growth performance and carcass yield. Thus, GM corn appears to be safe for use as a feed component for poultry.

Cattle. In beef cattle and lactating dairy cows, utilization of corn silage from Bt corn has been studied. Folmer et al. (2002) found that presence of the Bt trait in corn hybrids had no consistent effect on performance of growing steers. Russell et al. (2001) conducted a study on pregnant beef cows and found that there were no differences between the hay required to maintain body condition of cows supplemented with Bt or non-Bt control hybrids. In beef cattle fed Bt corn during the finishing phases, Kerley et al., (2001) and Petty et al. (2001) both concluded that the presence of Bt protein did not affect average daily gain or feed efficiency. In lactating cows, whole plant silage from glyphosate-tolerant corn hybrid (NK603) was used in a feeding trial to compare with non-transgenic hybrids. Milk production, milk fat, crude protein, milk urea N, percentage milk total solids and somatic cell count were unaffected by the treatments. Similarly, feeding silage and grain consisting of Bt corn (MON810) to lactating dairy cows did not affect the production efficiency and nutritional value of milk (Donkin et al., 2003).

Digestion of Transgenic DNA

The genetic material of life is carried by the deoxyribonucleic acid (DNA), a molecule consisting of smaller units called nucleotides. Genes are composed of linear groups of 1000 or more nucleotides and provide the blueprint for the production of specific proteins,

or expression of certain traits in an organism. On average, plant species contain between 20 and 50×10^6 genes (Beever and Kemp, 2000).

Animals acquire foreign plant DNA through oral consumption. The food consumed by animals is composed of proteins, carbohydrates, lipids, nucleic acids, vitamins and minerals, which vary in quantity. The quantity of DNA, however, in most food crops is generally less than 0.02% on a dry matter basis (Beever and Kemp, 2000). Because of this, estimating the quantity of DNA ingested by animals is difficult. In addition, there are other sources of DNA in the gut such as shed epithelial lining, bacteria and protozoa residing in the gut, and white blood cells. In a transgenic plant, it is estimated that the inserted gene constitutes less than 0.00016 to 0.00066% of the total genomic DNA (Beever and Kemp, 2000). Based on these figures, it would appear that consumption of DNA from a genetically-modified plant is negligible compared to the total DNA consumption.

The DNA from GM plants is composed of the same building blocks that make up nucleotides in non-GM plant DNA. Thus, they are degraded in the same manner in the gastrointestinal tract (Beever and Kemp, 2000). The mechanical process of mastication cleaves the DNA into small fragments. In addition, gastric enzymes and acids act on the DNA and aid in its digestion. The enzymes involved in the hydrolysis of DNA are DNase I and DNase II (Beever and Kemp, 2000). The enzyme DNase is found in the saliva, pancreatic secretions, liver and the secretions of the Paneth cells of the small intestine. Both of these enzymes are poorly characterized, *in vivo*. However, *in vitro* studies have shown that DNase I and II can cleave single and double-stranded DNA primarily at the 3′ end. (Beever and Kemp, 2000). *In vitro* studies, involving human intestinal simulations, showed that naked DNA is rapidly degraded by digestive enzymes. However, transgenic DNA in maize and

soya appeared to be able to survive the attack of DNase longer than naked DNA (Martín-Orúe et al., 2002). This could be due to the hypermethylation of plant DNA and its tight association with histones, and the presence of the plant cell wall which may provide protection against DNase action (Martín-Orúe et al., 2002).

Several studies have been conducted to investigate the fate of ingested DNA in the animal's body. Schubbert et al. (1997) found that ingested foreign DNA is not fully degraded in the gastrointestinal tract of mice fed a diet containing phage M13mp18 DNA as a test gene. Fragments of this gene were detected in the small intestine, cecum, large intestine and feces of mice. Furthermore, fragments of the M13mp18 DNA (up to 976 bp) were detected in the blood of 254 mice two to eight hours after feeding. Foreign DNA fragments were detected in the columnar epithelial cells of the intestine, leukocytes in the Peyer's patches of the cecum wall, in the liver cells, and in the B cells, T cells and macrophages from the spleen up to 18 hours post-feeding. This study suggests that fragments of foreign DNA, ingested orally, can pass through the small intestinal epithelia and may be carried by the blood to other organs in the body. Doerfler and Schubbert (1998) followed up this study to further investigate the fate of ingested foreign DNA in the gastrointestinal tract of mice and the possibility of transplacental transfer between pregnant mice and the fetus. This study further confirmed their previous work and showed that about one to two percent of ingested foreign DNA can survive passage through the gastrointestinal tract. They were also able to detect the M13 test DNA in some organs of the fetus and newborn mice, but not in all cells, indicating transplacental transfer. Results of experiments conducted by Hohlweg and Doerfler (2001) agreed with the abovementioned studies. In their study, mice were fed with soybean leaves

and the ribulose-1,5-bisphosphate carboxylase (Rubisco), a gene present in plants, was used as the test gene. They found that the Rubisco gene or fragments of it, could be detected from two to 49 hours after feeding in the intestine and up to 121 hours specifically in the cecum. This study suggested that plant-associated DNA is more stable in the intestinal tract than naked DNA.

Studies on the fate of DNA in the gastrointestinal tract suggest the possibility that transgenes, present in GM plants, could affect the growth of animals. Animal scientists are concerned whether the novel genes can be absorbed in the gastrointestinal tract and pose deleterious effects on livestock production. Chowdhury et al. (2003) conducted several studies to detect DNA fragments in several species of farm animals fed GM corn using polymerase chain reaction (PCR). In a study conducted in pigs fed StarLink CBH351 corn variety, it was found that the *cry9C* gene, both the 103 and 170 base pairs fragments, and the non-GM DNA were still detectable in the rectal and cecal contents. In a similar study using Bt corn Event 11, Chowdhury et al. (2003) detected the inherent DNA fragments and the *cry1Ab* gene (110 bp and 437 bp) in the gastrointestinal tract of pigs. Both of these studies imply that ingested DNA is not completely degraded in the gastrointestinal tract as demonstrated by the presence of PCR-detectable fragments. However, neither the non-GM DNA nor the *cry1Ab* gene fragments were detected when peripheral blood was examined, and this precluded conclusions about any potential absorption of the intact protein.

Fate of GM corn DNA in the rumen of sheep was investigated by Duggan et al. (2003). Using PCR, they found that the 1914 bp DNA fragment containing the entire coding region of the *cry1Ab* gene was still amplified from rumen fluid collected five hours after feeding corn grains. However, the same fragment was not detected in the rumen of sheep fed

silage prepared from GM corn. A shorter fragment (211 bp) was detected in the rumen fluid 3 h after feeding silage and 24 h after feeding corn grains. The findings suggest that DNA from corn grains survive for a longer period of time compared to DNA from silage.

In poultry, Jennings et al. (2003) investigated the presence of both transgenic and endogenous plant DNA in breast muscles of broilers fed YieldGard Corn Borer (MON 810) variety. Using PCR and Southern blot hybridization technique, the DNA samples extracted from the breast muscles were analyzed for the presence of a 211 bp fragment of Bt *cry1Ab* gene and a 213 bp fragment of the endogenous corn gene *sh2*. Neither of the two types of fragments were detected in the samples.

Digestion of Transgenic Proteins

In assessing the safety of genetically modified plants, the consequences and potential risks associated with the presence of expressed proteins are of particular concern. Dietary proteins are hydrolyzed in the lumen and in the mucosal cells of the gastrointestinal tract by the action of proteases and peptidases that cleave the peptide bonds. The pancreas secretes proteases into the duodenum, namely trypsinogen, chymotrypsinogen (endopeptidases) and carboxypeptidase A and B (exopeptidase). Their action on proteins results in the production of free amino acids, dipeptides and tripeptides which are absorbed by the enterocytes via specific carrier systems and are carried to the liver by way of the portal blood (Argenzio, 1993).

Digestibility studies have been conducted by exposing the proteins of interest to simulated gastric fluid (SGF) containing pepsin for various periods of time followed by determination of protein or protein fragments by SDS-PAGE and western blots. The crystal proteins *Cry34Ab1* and *Cry35Ab1*, expressed in *Bacillus thuringiensis Berliner* were found to

be rapidly digested in SGF (Herman et al., 2003). In vitro digestion of the CP4 EPSPS protein in glyphosate-resistant soybeans showed that the protein is broken down rapidly by proteolytic enzymes (Harrison et al., 1996). This indicates that this protein is broken down with relative ease in the gastrointestinal tract, demonstrating that consumption of transgenic proteins poses no potential harm to animals.

Carcass and Meat Quality Definitions and Measurement

Defining quality as it relates to carcass and meat involves different parameters. Carcass quality often describes the yield of lean meat and fat thickness, while meat quality describes appearance and functional characteristics (Wood, 2001). The parameters that are measured may include, but are not limited to, carcass pH and temperature, color, water-holding capacity, and tenderness. Consumers are the ultimate decision makers of meat quality, and their perception of the product will influence their buying behavior.

Temperature and pH. The lowering of pH in muscle, post-slaughter, is due to the accumulation of lactic acid when muscle glycogen is metabolized by anaerobic glycolysis in an attempt to maintain homeostasis (Maltin et al., 2003). Muscle pH normally declines from a pH 7.4 in living muscle to a pH of about 5.6 to 5.7 within six to eight hours, post-mortem. An ultimate pH of about 5.3 to 5.7 is reached at approximately 24 hours post-slaughter (Hedrick et al., 1993). Meat quality is affected when acidic conditions (low pH) in the muscle develop early as a result of lactic acid accumulation. Muscle proteins denature when acidic conditions are achieved before the heat of the carcass, generated from ongoing metabolism and scalding, is dissipated through carcass chilling (Maribo et al., 1998). Denaturation of proteins results in loss of water-holding and protein-holding capacities, and loss in intensity

of muscle pigments (Hedrick et al., 2003). Lower temperature decreases the rate of anaerobic metabolism and the subsequent accumulation of lactic acid in the muscle after exsanguination (Maribo et al., 1998).

A model rate of pH decline for normal pork is approximately 0.01 units per minute (Offer, 1991). Very rapid decline in pH (0.1 unit per minute) will result to meat that is pale, soft, and exudative (PSE) because of low water-holding capacity (Offer, 1991). Conversely, muscles that maintain a high pH, post-slaughter, will result in meat that is dark, firm, and dry (DFD).

Color. Color is an important parameter of meat quality because it provides the first impression consumers will have of a meat product, and is a deciding factor in making a purchase (Hunt et al., 1991). Uncooked meat color is usually described as pink or red, however, colors range from nearly white to dark red. Lack of redness in meat is easiest to determine because colors associated with discoloration of meat (tan, brown, gray, green or yellow) are difficult to measure instrumentally (Hunt et al., 1991).

Fresh meat color is dependent on myoglobin and its oxidative status (Van Oeckel et al., 1999). Myoglobin is a water-soluble protein that stores oxygen for aerobic metabolism in the muscle. It consists of a protein portion and a non-protein porphyrin ring with a central iron atom, which plays an important role in meat color (Hedrick et al, 1993). The oxidation state of iron and the type of compound attached to it, affects the color of meat. When meat is cut, oxygen from air comes in contact with the exposed meat surfaces and binds the iron. The surface of the meat blooms as myoglobin is oxygenated, resulting in oxymyoglobin. The latter pigment is commonly known as the fresh meat color (bright red), and is the most

desirable color of fresh meats. Myoglobin and oxymyoglobin have the capacity to lose an electron which turns the pigment to brown color and yields metmyoglobin (Young and West, 2001).

Several methods are available in measuring meat color. The use of the Hunter Lab-values, also known as L, a, and b values, is one of the most commonly used method involving meat products. L-values correspond to the lightness of a product, with zero indicating black and 100 indicating white. The a-values indicate the degree of redness (positive value) to greenness (negative value) of a product. The b-values measure the degree of yellowness (positive value) to blueness (negative value) (Hunt et al., 1991).

Water-holding capacity. The ability of meat to retain water during application of external forces such as cutting, heating, grinding or pressing, is referred to as water-holding capacity (Hedrick et al, 1993). Water may be lost by evaporation, drip, or cooking, and such losses contribute to meat shrinkage (Offer and Knight, 1988). Poor water-holding capacity (WHC) in muscle tissues will result in greater shrinkage. Thus, WHC is an important meat quality parameter to examine because losses in water affect the financial value of the product. In addition, the proper protein to water ratio is important for palatability and overall yield of the product (Hedrick et al., 1993). Drip losses occur when red aqueous protein solution, or sarcoplasmic fluid, oozes out from cut meat (Offer and Knight, 1988). This loss not only affects the weight (value) of the meat, but also affects its appearance and appeal to consumers because of liquid accumulating around the meat which is displeasing. In cut meat, such as steaks and chops, drip losses of about two to six percent can occur after chilling for four days (Zarate and Zaritzky, 1985 as cited by Offer and Knight, 1988). As a target for

pork quality, the National Pork Producers Council suggested a drip loss target of ⩽ 2.5% (NPPC, 1998). One method used in determining drip loss is by taking pieces of meat and enclosing it in a plastic bag to catch the drip and prevent evaporation (Offer and Knight, 1988).

Water molecules are polar, thus, they associate with electrically-charged reactive groups of muscle proteins. The drop in pH, postmortem, can reduce the number of reactive groups of proteins available for water binding because it approaches the isolectric point of myofibrillar proteins (Hedrick et al, 1993). At this point, the number of positively and negatively charged groups are equal and they tend to be attracted to each other instead of binding to water. Hence, a lower meat pH will result in greater loss of water.

Tenderness. Meat tenderness is influenced by the myofibrillar structure of the muscle, the amount of collagen or connective tissue proteins, the degree of muscle shortening after slaughter, and the extent of postmortem tenderization (Young and Gregory, 2001). The first two factors cannot be manipulated post-slaughter, and are dependent on the muscle's role in the live animal and on animal's age. The shortening of muscle fibers is due to the development of irreversible cross-bridges between myosin and actin as a result of biochemical processes that occur in an attempt to establish homeostasis at post-mortem (Maltin et al., 2003). Post-mortem tenderization of meat involves degradation of certain proteins due to some retained proteolytic activity in the muscle (from calpains and/ or cathepsins) which causes fragmentation of myofibrils, and increase in tenderness during ageing (Huff-Lonergan et al., 1996, Young et al., 2001, Maltin et al., 2003).

Meat tenderness may be measured using several methods, and these include Warner-Bratzler shear, star probe, and trained sensory panel (Lonergan and Prusa, 2002). The choice of method usually depends on the investigator and the resources available. Trained sensory panels involve a group of people who are trained to evaluate the product for tenderness or chewiness using a ten-point scale. Test for Warner-Bratzler shear involves the use of cooked chops from which 1.27-cm core samples are taken for testing instrumental tenderness using a Warner-Bratzler shear attached to a Texture Analyzer. The star probe procedure is another method of measuring instrumental tenderness, and involves the use of a circular, five-pointed star probe attached to an Instron Universal Testing Machine (Lonergan and Prusa, 2002). Lonergan, et al. (2001) found that Warner-Bratzler shear and star probe measurements were highly correlated and can be used in predicting sensory properties of tenderness in pork.

Effect of Sex and Slaughter Weights on Growth and Carcass Characteristics

The effect of increasing slaughter weight on growth and meat quality of individually-housed male castrates, boars, and gilts was investigated by Weatherup et al. (1998). Individually-housed boars, barrows, and gilts did not differ in feed efficiency when slaughtered at less than 90 kg, but gilts and barrows had poorer feed conversion when harvested at 90 and 100 kg, respectively. The average daily gain for the whole period did not differ with increasing slaughter weight, despite increases in daily feed intake. Barrows had greater daily feed intake than boars and gilts, but gilts had a lower daily gain. Barrows had greater backfat depth than boars and gilts. Meat quality measures such as pH, drip loss, and Warner-Bratzler shear force were not affected by slaughter weight. CIELAB color parameter (L*, a*, b*, chroma, hue) were likewise unaffected by slaughter weight. However,

Weatherup et al. (1998) found increases in crude protein (CP) and fat content with increasing slaughter weight. Gilts were found to have greater CP content of the *longissimus dorsi* compared to barrows and boars. The investigators concluded that meat quality is maintained at heavier slaughter weights.

Overall growth rates and feed efficiencies of pigs were unaffected by sex and slaughter weight between 100 and 160 kg (Cisneros et al., 1996). However, dressing percentage increased linearly by 0.32 percentage units per 10-kg increase in slaughter weight. Gilts had lesser 10^{th} rib fat and larger loin eye area than barrows, but overall backfat deposition did not increase with slaughter weight. Meat quality measures such as pH, drip loss, shear force, moisture and fat content, did not differ between sexes. Increasing slaughter weight was associated with lower carcass 24-h pH and an increase in drip loss by 0.3% for every 10-kg increase in weight. The findings suggest that limited changes in some meat quality parameters occur with increased slaughter weight.

Peinado et al. (2003) reported limited effects of sex and slaughter weight (114 kg and 122 kg) on pork quality. Shear force was found to be greater for heavier pigs. Meat from females had greater L* and b* values than meat from males, but meat color was not affected by slaughter weight. Protein and fat content of the loin, drip and cooking losses, were likewise not affected by slaughter weight.

Lawlor et al. (2003) found that average daily gain (ADG) was not affected by sex but feed conversion ratio (FCR) was greater in barrows than gilts. Pigs were divided into five slaughter weights (80, 90, 100, 110, and 120 kg), and a linear effect was observed for ADG and FCR with increasing weight. Backfat depth was greater in barrows than gilts, and also showed a linear response with increasing slaughter weight.

In a study conducted by Latorre et al. (2004), average daily feed intake (ADFI) and ADG of barrows were greater than those of gilts, but feed efficiency was greater in gilts. Pigs slaughtered at 116 kg had greater ADG than pigs slaughtered at 124 and 133 kg, although increasing slaughter weight did not affect daily feed intake. Pigs harvested at 116 and 124 kg converted feeds better than those harvested at 133 kg. Barrows had lower dressing percentages and produced fatter carcasses. Dressing percent and backfat depth increased as slaughter weight increased. Sex affected carcass pH, with barrow carcasses having higher 45-min pH and 24-h pH than gilt carcasses. The 45-min pH was higher in pigs slaughtered at 133 kg, however, 24-h pH was not affected by slaughter weight. Shear force values were greater in gilts than in barrows. Sex, however, had no effect on moisture, lipid content, and color of the longissimus muscle. Lower L* and higher a* values were observed in pigs slaughtered at 133 kg. The study suggests that increasing the slaughter weight had a negative effect on live pig performance and does not offer any major benefit on the quality of pork.

The effect of slaughter weight on carcass characteristics of Yorkshire barrows and gilts was investigated by Fortin (1980). Four slaughter weights were used (85, 92, 103, 112 kg) to determine the effect on selected carcass measures. Hot carcass weight and chilled carcass weight increased linearly with increasing slaughter weight. Dressing percentage, however, was not affected by slaughter weight or sex.

Ellis and Avery (1996) found that growth rate remained constant across three slaughter weights (90, 110, 130 kg), but FCR showed a steady increase with increasing slaughter weight. Fat depths and loin eye area increased with increasing slaughter weight.

Nitrogen and Phosphorus Excretion in Pigs

Impact of N and P in the environment. In the past couple of decades, animal agriculturists have realized the environmental concerns associated with the modernization of animal production. In many countries, disposal of manure and control of odor are very important issues that warrant serious attention. Traditionally, swine producers and nutritionists have focused on the goal of maximizing the performance of the animal. To accomplish this, diets were most often formulated to contain excess amounts of nutrients to be on the "safe" side, with little or no consideration to the nutrients excreted to the environment. At present time, more nutritionists are aware of nutrient management, and the need to formulate pig diets based, not only on animal performance and profitability, but also on minimizing nutrients excreted and odors produced.

Swine production operations have increased over the past years and have become more integrated, posing more challenges. Although the number of farms have decreased in recent years, the size of farm operations have increased; farm operations have, thus, become more concentrated in land area (Hollis and Curtis, 2001). When more nutrients in manure are excreted, more land is needed to accommodate the spreading of manure. Land application of manure is an efficient means of recycling nutrients because manure contains valuable nutrients such as nitrogen (N) and phosphorus (P). Nutrients in manure help build and maintain soil fertility (Ribaudo et al., 2003). However, excess N and P can negatively affect the quality of surface and ground water. Nitrogen in excess can increase the nitrate content of groundwater and can lead to runoff of nitrates in surface water. Likewise, excess P can result in buildup in the soil which may eventually lead to movement of phosphorus into bodies of water when soil erodes (Correll, 1999). Through the process of eutrophication, growth of

aquatic vegetation, such as algae, is accelerated in the presence of N and P, and decomposition of such vegetation can negatively alter water quality (Sharpley et al., 1994). For these reasons, N and P are used as basis for most nutrient management planning (Kornegay and Verstegen, 2001; Powers and Van Horn, 2001).

Pigs consume N in the form of protein. Phosphorus is consumed in organic (plant or animal origin) and/ or inorganic (e.g. dicalcium phosphate) forms. Phosphorus from plant origin is bound in a molecule called phytate, and its release would require the enzyme phytase. Pigs, however, do not have sufficient quantities of the enzyme phytase (Reese and Koelsch, 1999). The quantity of N and P excreted by pigs can be affected by several factors, including source, quality, amount of N and P consumed, proportions of other nutrients consumed, the proportions of N and P consumed that are used for growth and reproduction, the amount of N and P represented by endogenous losses due to sloughed cells and bacteria in the gut, processing methods, age, and nutritional status of the animal (Kornegay and Verstegen, 2001; Reese and Koelsch, 1999). Digestibility estimates of common feeds may be used in estimating and predicting the amount of N and P to be excreted by livestock animals. Nutrient excretion may be calculated from known values of nutrient intake of an animal and the nutrient content in their excreta. (Powers and Van Horn, 2001).

Apparent digestibility of N and P. Apparent digestibility is defined as the difference between the amount consumed and the amount collected in the feces. Estimates of apparent digestibilities of N and P in feed ingredients such as corn and in pig diets have been well studied. The estimates vary between different studies and this may be due to the differences in experimental methods and analysis. In a review, Kornegay and Harper (1997) cite that growing-finishing pigs fed commercial feedstuffs digest 75-88% of N and 20-70% of P

consumed. It was estimated that less than 15% of P is bioavailable in pigs because about 70% of the total P in grain is in the form of phytate which is poorly available to pigs (NRC, 1998). Weremko et al. (1997) presented a review of the bioavailability of P in feeds of plant origin for pigs. In their summary of findings, apparent digestibility of P ranges from 12-23% in corn, and 29-39% in corn-soybean meal diets. Spencer et al. (2000), investigated the digestibility of diets containing normal and genetically-modified low phytate corn. Results of their experiment showed that P digestibility in diets containing non-GM corn with and without additional 0.2% dicalcium phosphate was 46% and 16%, respectively ($P < 0.01$). In diets with low-phytate corn, P digestibility was 48% and 54%, with 0 and 0.2% additional dicalcium phosphate, respectively ($P < 0.01$). Nitrogen digestibility is about 86%, and was not significantly different between diets.

In pigs fed high available phosphorus corn (HAP), Sands et al. (2001) found that P digestibility and retention was improved in groups fed HAP, and the P excreted was reduced compared to conventional corn. The digestibility of P in HAP diets and conventional corn diets were 53% and 38%, respectively ($P < 0.05$). Digestibility of N, was around 91% ± 1.66 and was not significantly different between treatments.

Nitrogen digestibility in pigs fed high-oil corn was 76% ± 1.45 in diets consisting of 97% of one of the four varieties of corn tested (one conventional and three high-oil corn). In corn-soybean meal diets (79% of one of the four corn varieties + soybean), N digestibility was 79% in the conventional corn diet and 82-85% ($P < 0.05$) in diets containing high-oil corn (Adeola and Bajjalieh, 1997).

Nitrogen metabolism in gilts fed standard corn-soybean meal diets or low-crude protein diets supplemented with amino acid was investigated by Figueroa et al. (2002). Gilts

were fed with rations formulated to contain different levels of crude protein, with or without amino acid supplements (18%, 14% + AA, 16%, 12% + AA, 14%, and 10% + AA). Results showed that N intake decreased linearly as protein in the diets decreased. Decrease in nitrogen excreted, which ranged from 5.81 to 4.36 g/d in feces reflected the decrease in N intake. Apparent digestibility of N was significantly greater in standard diets than in AA-supplemented diets. In standard diets, apparent N digestibility increased as the levels of crude protein decreased, and values ranged from 87-88%. In AA-supplemented diets, apparent N digestibility ranged from 83-86% and showed a decreasing trend as the level of CP decreased. Nitrogen retention, expressed as percentage of N intake, ranged from 58-62% and was not affected by dietary protein concentration and AA supplementation.

Summary

Genetic modification in crops for herbicide tolerance and insect resistance offers great agronomic benefits and their significance is expected to increase in the future. Because corn is a major component of feed in growing-finishing swine, animal nutritionists are confronted with the question of whether genetic modification in corn could result in unintended alterations in the nutritive value, and hence, affect pig production in a negative manner. Previous studies involving genetically modified corn in pigs have been limited and have focused on varieties other than Bt 11, which possess both herbicide and insect resistance. Therefore, the objective of this study was to compare the growth performance, carcass quality, and excretion characteristics of pigs fed diets containing either Bt 11 corn (Syngenta Seeds, Inc) or non-genetically modified corn. Feeding trials are necessary to establish substantial equivalence between GM and non-GM feed ingredients used for livestock, and ultimately to establish the safety of foods of animal origin.

CHAPTER 3. MATERIALS AND METHODS

Animals

All procedures for this project were in accordance with the Iowa State University Animal Care and Use Committee guidelines. The experiment was conducted at the Iowa State University Bilsland Research Farm in Madrid, Iowa from Feb 18 to April 17, 2003. Sixty-four Yorkshire pigs, consisting of 32 barrows (castrates) and 32 gilts (average initial body weight of 64 kg and 60 kg, respectively) were used in this experiment. The pigs were allocated into 16 pens (4 pigs/pen) according to size and gender, providing the same animal profile between treatments. Each pen was assigned to either a diet with Bt corn or a diet with the control corn.

Housing

Pigs were housed in an environmentally-controlled building with 16 concrete-floored pens. Pen dimensions (length × width) were 3.5 × 2.3 m, providing a floor space of 2.01 m^2 pig^{-1}. The temperature in the building was maintained at approximately 30 °C using a thermostat-controlled heater (White Heater Model 346E, L.B. White Co, Inc., Onalaska, WI). Each pen was provided with one nipple drinker and one Smidley-Ranger self-feeder (Marting Manufacturing of Iowa, Inc., Britt, IA). Entry to the building required observance of biosecurity protocols imposed in the farm.

Feeding

The Bt Event 11 (Syngenta Seeds, Inc.) was used in this study and the control diet was composed of combined corn grains from a number of non-genetically modified inbred lines. Each type of diet was further divided into gilt and barrow diets to suit the differences in the nutrient requirements between male and female animals. The diets were referred to as

control-gilt (C-G), control-barrow (C-B), Bt-gilt (Bt-G), and Bt-barrow (Bt-B). There were four pens assigned to each of the four diets (n = 4 pigs per pen).

The composition of diets was adjusted as the experiment progressed, based on the growth phase of the animals. There were a total of three phases for the duration of the experiment. Preliminary analysis of the corn grain showed difference in crude protein (CP) content between control and Bt corn, with the control corn having a greater CP content (8.71% vs. 7.45%; Table 2). This was taken into account during feed formulation, hence, control and Bt diets were formulated to be isocaloric and isonitrogenous. The composition of diets in each phase is listed in Table 3. The diets were formulated to meet the estimated NRC requirements for growing pigs (NRC, 1998). All diets contained Celite 281® (World Minerals, Inc., Santa Barbara, CA), an inert, indigestible diatomaceous earth that is used as a marker to determine nutrient digestibilities (Vogtmann et al., 1975).

Table 2. Nutrient content of corn grains (preliminary analysis[a]).

Item (%)	Control corn[b]	Bt corn[c]
Moisture	11.05	11.49
Fat	3.27	3.01
Protein	8.71	7.45
Fiber	1.9	2.0
Ash	0.95	1.10
Tryptophan	0.07	0.06
Cystine	0.22	0.21
Methionine	0.18	0.16
Aspartic acid	0.63	0.55
Threonine	0.31	0.27
Serine	0.41	0.35
Glutamic acid	1.60	1.33
Proline	0.69	0.60
Glycine	0.32	0.29
Alanine	0.62	0.52
Valine	0.38	0.32
Isoleucine	0.28	0.23
Leucine	0.99	0.81
Tyrosine	0.20	0.18
Phenylalanine	0.39	0.33
Lysine, total	0.27	0.25
Histidine	0.24	0.21
Arginine	0.36	0.32

[a]Analysis conducted by Woodson-Tenent Laboratories, Inc., Goldston, NC.
[b]Control corn consists of combined grains from a number of non-genetically modified inbred lines.
[c]Bt corn = Bt 11 (Syngenta Seeds, Inc)

Table 3. Ingredients and nutrient composition of diets[a], as formulated.

Ingredient (%)	*Phase 1 (60-80 kg)*				*Phase 2 (81-90 kg)*				*Phase 3 (91-110+ kg)*			
	C-G	C-B	Bt-G	Bt-B	C-G	C-B	Bt-G	Bt-B	C-G	C-B	Bt-G	Bt-B
Corn[b,c]												
control	77.50	83.00	-	-	77.60	77.00	-	-	81.00	83.00	-	-
Bt corn	-	-	78.00	82.30	-	-	77.60	77.00	-	-	83.00	83.00
Soybean meal	15.70	11	15.95	11.70	12.50	9.60	13.05	10.10	9.90	8.75	9.30	9.30
Salt	0.25	0.25	0.25	0.25	0.25	0.25	0.25	0.25	0.25	0.25	0.25	0.25
KSU trace mineral mix[d]	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10
KSU trace vitamin mix[e]	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10	0.10
Calcium carbonate	0.99	1.00	0.93	0.93	0.98	1.01	0.92	0.94	1.04	1.05	0.97	0.97
Dicalcium phosphate	0.53	0.33	0.64	0.45	0.40	0.26	0.51	0.38	0.24	0.19	0.31	0.31
Celite	1.17	1.02	1.03	0.97	1.57	1.98	1.42	1.88	1.47	1.06	0.95	0.95
Sucrose	3.66	3.20	3.00	3.20	6.50	9.70	6.05	9.25	5.90	5.50	5.02	5.02
Total	100.00	100.00	100.00	100.00	100.00	100.00	100.00	100.00	100.00	100.00	100.00	100.00
Formulated analyses												
ME, kcal/kg	3,298	3,306	3,298	3,307	3,303	3,309	3,304	3,309	3,320	3,320	3,320	3,320
CP	14.00	12.00	14.00	12.00	12.00	11.00	12.00	11.00	11.00	11.00	11.00	11.00
Lysine	0.68	0.56	0.68	0.56	0.59	0.50	0.59	0.50	0.52	0.49	0.49	0.49
Total P	0.44	0.38	0.48	0.43	0.39	0.34	0.44	0.39	0.35	0.34	0.39	0.39
nPP	0.19	0.15	0.19	0.15	0.16	0.13	0.16	0.13	0.13	0.12	0.12	0.12
Lysine, analyzed	0.74	0.64	0.72	0.67	0.60	0.53	0.60	0.61	0.74	0.58	0.71	0.64
Methionine, analyzed	0.29	0.29	0.28	0.27	0.25	0.24	0.28	0.26	0.28	0.24	0.26	0.26
Threonine, analyzed	0.59	0.53	0.55	0.52	0.51	0.46	0.53	0.48	0.58	0.50	0.53	0.49
Total P, analyzed	0.41	0.36	0.39	0.38	0.37	0.38	0.43	0.38	0.43	0.28	0.40	0.37

[a]C and Bt indicate corn source (control and biotechnology-derived); G and B indicate gilts and barrows, respectively.
[b]Corn source = combined grains from a number of non-genetically modified inbred lines.
[c]Corn source = Bt 11 (Syngenta Seeds, Inc.).
[d]Trace Mineral Premix: Cu (1.1%; as copper sulfate), Zn (11%; as zinc oxide), Mn (2.6%; as manganous oxide), Fe (11%; as iron sulfate), I (198 ppm; as ethylene diamine dihydriodide), Se (198 ppm; as sodium selenite);
[e]Swine Vitamin Premix: Vit. A (2,000,000 IU/lb); Vit. D3 (300,000 IU/lb); Vit. E (8,000 IU/lb); Menadione (800 mg/lb); Vit. B12 (7 mg/lb); Niacin (9,000 mg/lb); Panthothenic acid (5,000 mg/lb); Riboflavin (1,500 mg/lb).

Data Collection

Pigs were allowed *ad libitum* access to feed and water throughout the duration of the study. To minimize feed wastage, feeders were filled daily so that the following day, the amount of feed left was just enough to cover the bottom of the feeder. Feeders were checked daily and adjusted accordingly such that the amount offered each day was estimated to be 10% greater than the anticipated consumption for that day. The amount of feed offered to each pen was recorded daily and feed disappearance was determined weekly. The amount of feed remaining in the feeder at the end of each week was subtracted from the total feed offered during the week to estimate the total feed consumed. Pigs were individually weighed weekly, using an electronic scale (Model T1-1000 W/ BATT, Transcell Technology, Inc., Ackley, IA). Average pen weight was calculated weekly.

Collection of Feed, Fecal and Urine Samples

Fecal and urine samples were collected from each pig on a weekly basis throughout the duration of the study. Because the pigs were not in metabolism crates, total 24-h collection of feces and urine was not possible. Instead, grab samples were collected from each pig by catching feces and urine, as voided, using plastic containers. Fecal samples for each pen were pooled using approximately 50 g of feces from each pig. The samples were dried in aluminum pans, in a forced-air oven (55 °C). Dried feces were ground using a Thomas-Wiley Intermediate Mill (3383-L10 series Thomas Scientific, Swedesboro, NJ) with a 20 mesh sieve and stored until analyses. The urine samples were pooled, by pen, using the same amount from each pig, approximately 20 ml, but depended on the amount of urine collected during that week. Pooled urine samples were transferred to 50-ml capacity plastic tubes with caps and frozen until analyses.

Feed samples were collected from each pen and then pooled by diet. There were two collections for each phase of the diet. Samples were sent to Dairy One Forage Testing Laboratory (Ithaca, NY) for proximate and mineral analyses and to Experiment Station Chemical Laboratories, University of Missouri (Columbia, MO) for amino acid analyses. Feed samples were also stored until analyses for nitrogen (N), phosphorus (P), dry matter (DM), and acid insoluble ash (AIA).

Harvest Schedule

Pigs were divided equally into two harvest groups based on market weight. Half of the pigs in each dietary treatment group (Bt, Control) were harvested at an average market weight of 85 kg. The other half were harvested at an average market weight of 100 kg. Originally, it was planned to grow the other half to 120 kg. However, due to limitations in the supply of corn used in the experiment, the pigs were grown to a target weight of 100 kg. Due to capacity limitations in the harvest facility, the pigs from each harvest group were further divided into two slaughter dates, two d apart. As a result, there were 16 pigs (8 from Bt, 8 from control treatments) at each slaughter date. The pigs were brought to the Iowa State University Meat Laboratory, fasted overnight, and were slaughtered the following day using approved humane practices (USDA/ FSIS Directive 6900.2). Hot carcass weights were recorded before chilling. The time interval between exsanguination and chilling of each of the carcasses was also recorded.

Carcass measurements

Carcasses were chilled for 24 h in a forced-air cooler at -5 °C. The drop in the temperature of the carcasses was recorded at 1, 6, and 24 h post-slaughter using a digital probe thermometer (Thermocouple Thermometer Model 600-1040, Barnant Co., Barrington,

IL). Likewise, carcass pH was measured using a pH meter with a glass body penetration probe (pH-STAR Pistol Model 5000, SFK Technology Inc., Cedar Rapids, IA) at the same time points. Both temperature and pH measurements were obtained from the area of the *longissimus dorsi* at the 12th rib on the right side of the carcass. Loin eye area and backfat thickness (1st rib, 10th rib, last rib, and last lumbar vertebrae) were measured 24 h post-slaughter.

Collection of Loin Samples

Boneless loin samples were collected 24 h post-slaughter. Samples were obtained from the *longissimus dorsi* of the left side of the carcass. From each of the carcasses, three 2.54-cm thick loin chops were collected for color analysis, which was performed approximately 1 h after collection. These same chops were used for analysis of drip loss after color analysis had been conducted. Two 2.54-cm thick chops were collected for star probe analysis. One 2.54-cm thick sample was collected for proximate analyses. The samples for proximate analyses were frozen immediately after vacuum packing. The loin samples for the star probe analysis were vacuum-packed and aged for 7 d at 2 °C. After the aging period, the samples were stored frozen at -20 °C until the analyses.

Laboratory Procedures

Color. Meat color was measured from fresh 2.54-cm thick loin chops using HunterLab LabScan Instrument (Hunter Associates Laboratories, Inc., Reston, VA). There were three loin chops per carcass and the samples were kept chilled during the procedure by putting them on a tray with ice underneath. The instrument parameters were set as follows: Illuminant = D65; Observer = 10°; Port size = 2.54 cm (Hunt, et al, 1991). Two readings

were recorded from each chop. Values for L (lightness), a (red-green scale), and b (yellow-blue scale) were reported as the average of six readings from the three chops.

Drip loss. The chops used for the color analysis were used for analysis of drip loss. The samples were pat-dried using paper towels and their individual initial weight recorded. The chops were placed separately in Ziploc® bags and stored at 4 °C for 7 d. Final weight of each sample was measured on the seventh day. The following formula was used to calculate the percentage drip loss:

$$\%\ Drip\ loss = \frac{(Initial\ sample\ weight - Final\ sample\ weight)}{Initial\ sample\ weight} \times 100$$

The values were reported as the average of three chops per carcass.

Tenderness (Star Probe). The loin samples were thawed at 2 °C and the remaining fat layer surrounding the chops was removed. Samples were broiled in an electric range (Amana Model Distinction, Amana Appliances, Amana, IA) to an internal temperature of 30 °C, turned and further cooked until an internal temperature of 64 °C was reached. The distance of the chops from the heat source was approximately 9 cm. The internal temperature was monitored using a digital thermometer (Model 115-KC-DSS, Omega Engineering, Inc., Stamford, CT) with attached thermocouples (Chromega/Alomega, 0.02 diameter, 72 inches, Model 5TC-GG-K-24-72, Omega Engineering, Inc., Stamford, CT). The cooked loin chops were allowed to cool to room temperature. The texture of the chops were determined using a circular, five-pointed star probe attached to an Instron Universal Testing Machine (Model 4502, Instron Corp., Canton, MA). The diameter of the probe is 9 mm with 6 mm between each point. The angle from the end of each point up into the center of the probe is 48°. The following settings were used for all the samples: a load cell of 10 KN; the crosshead speed

was set to 200 mm/min; the probe was lowered 35.21 mm; dwell time was five sec. The star probe was set to determine the amount of force needed to puncture and compress the chop to 80% of its height. Values were reported as an average of six punctures, three from each of the two loin chops from each carcass.

Proximate analyses of meat samples. Loin samples collected for proximate analyses were thawed at 2 °C. After thawing, the remaining fat layer was removed and each sample was ground using a food processor (Sunbeam Oskar®/ Sunbeam/ Oster Household Products, Niles, IL). The procedure used was according to the approved method for moisture (forced-air oven drying method, AOAC method 950.46), and crude fat analysis (ether extract method, AOAC method 960.39) for meats. The following equations were used to calculate the percentage moisture and fat content of the meat samples:

$$\%\,Moisture = \frac{(Sample\,wet\,weight - Sample\,dried\,weight)}{Sample\,wet\,weight} \times 100$$

$$\%\,Fat = \frac{(Sample\,dried\,weight - Sample\,extracted\,weight)}{Sample\,dried\,weight} \times 100$$

Values for percent moisture and fat were reported as the average of two replicates per sample.

Crude protein content of the ground meat samples was determined by a combustion method (AOAC method 992.15) using a Leco FP-428 Nitrogen Determination System (Leco Corporation, St. Joseph, MI) with software version 2.1. Values were reported as average of 2 replicates per sample.

Analyses of Feeds, Feces and Urine. Dried and ground feed, fecal samples and thawed urine samples were analyzed for N by Kjeldahl method (AOAC method 955.04,

modified to fit the FOSS Tecator® procedure). This involved digestion of samples with sulfuric acid and ST- Auto Kjeldahl tablets as catalysts (1.5 g potassium sulfate and 0.015 g selenium), followed by distillation using Kjeltec System 1002 Distilling Unit (FOSS Tecator AB, Höganäs, Sweden). Phosphorus content of feed and feces was analyzed using AOAC method 973.55, involving digestion of sample using HCl and nitric acid, followed by spectrophotometry using Hach® DR/4000 Spectrophotometer at 400 nm absorbance (Hach Co., Loveland, CO). Dry matter content of feed and feces was determined by drying at 100°C in a forced-air convection oven (Precision, Winchester, VA) for 24 hours. Acid insoluble ash (AIA) was analyzed by digesting the sample with HCl and ashing at a muffle furnace (Isotemp®, Fisher Scientific, Pittsburgh, PA) at 600°C for 5 hours (Vogtmann et al., 1975). The total fecal output per pen per week and apparent digestibility of N and P, were calculated using the AIA concentration in diets and feces. The following formulae were used:

$$Celite\ consumed\ per\ week\ (g) \quad = \quad Feed\ consumed\ per\ week\ (g) \times \%\ Celite\ in\ diet$$

Assume: Celite intake = Celite in feces

$$\frac{Celite\ consumed\ per\ week\ (g)}{\%\ Celite\ in\ feces} \quad = \quad Total\ feces\ per\ week\ (g)$$

$$Apparent\ Digestibility\ (\%) = 100 - ((AIA_D / AIA_F)\ (N_F / N_D)\ x\ 100)$$

where: N_F and N_D are the amount of each component (N or P) in feces and diet, respectively; and, AIA_F and AIA_D are the amount of Celite® as determined by acid insoluble ash in feces and diet, respectively. Results for feed intake and total feces per week were converted into per day basis for reporting.

Statistical Analyses

The pen was considered the experimental unit. Variables were analyzed as a 3×2 factorial design using the GLM procedure of SAS (SAS Institute, Inc., Cary, NC). The fixed effects included in the model were corn source (Bt vs. control), gender (barrows vs. gilts), slaughter weight (85 kg vs. 100 kg), gender and corn source interactions, slaughter weight and corn source interactions, and gender and slaughter weight interactions. Values were reported as least squares means from the PDIFF and STDERR options of SAS. Statistical significance was declared at $P < 0.05$.

CHAPTER 4. RESULTS

Growth Performance

Average daily feed intake (ADFI), average daily gain (ADG) and feed conversion ratio (FCR) of pigs in each treatment are shown in Table 4. There were no significant treatment effects for ADFI and ADG. Feed conversion ratio (unit feed: unit gain in weight) was greater in pigs fed diets containing Bt corn, (3.34 vs. 3.23), suggesting that pigs fed diets with the control corn were more efficient feed converters (P = 0.003). At the start of the experiment, the average weight of the gilts was 4 kg less than the average barrow weight (63 kg vs. 59 kg). At the conclusion of the experiment, the barrows were, on average, 7 kg heavier than gilts (99 kg vs. 92 kg; P = 0.0002). Gender had an effect on ADG, with barrows gaining 91 g/day more than gilts (P = 0.006). However, FCR was greater (P < 0.0001) for barrows (3.41) compared to gilts (3.17), indicating that gilts were to be more efficient feed converters compared to barrows.

Table 4. Effects of corn line and gender on growth performance of growing-finishing swine.

Parameter[a]	Dietary treatments[b,c]				*P*-values			SEM
	C-G	C-B	Bt-G	Bt-B	Treatment	Gender	Treatment × Gender	
Initial weight	58.71	63.05	59.45	63.42	0.53	<.0001	0.83	0.88
Final weight (kg)	92.84	100.02	92.19	99.54	0.75	0.0002	0.96	1.82
ADFI (kg)	2.28	2.77	2.31	2.78	0.91	0.0001	0.97	0.07
ADG (kg)	0.733	0.828	0.717	0.803	0.53	0.0060	0.88	0.032
FCR (feed:gain)	3.11	3.35	3.22	3.46	0.003	<.0001	0.94	0.03

[a]ADFI: average daily feed intake; ADG: average daily gain; FCR: feed conversion ratio
[b]C and Bt indicate corn source (control and biotechnology-derived); G and B indicate gilts and barrows, respectively.
[c]4 pigs per pen; 16 pigs per treatment

Pigs were fed three diet phases over the course of the experiment. There were no significant interactions between corn line and gender for any of the parameters at any phase

(Table 5). During phase 1 of the feeding trial, ADG was greater (P = 0.01) in pigs fed diets with control corn than those fed Bt diet (822 g vs. 682 g). This difference, however, was not observed during phases 2 and 3 and the overall ADG did not differ between treatment groups (P = 0.52; Table 5). There were no significant differences in the ADFI between treatments during phases 1 to 3. There were significant differences in FCR between treatments during phases 1 and 2, although the pattern was inconsistent. Pigs fed diets with control corn converted feeds more efficiently than pigs fed diets with Bt corn in phase 1 (2.94 vs. 3.53; P = 0.01), whereas in phase 2, pigs fed diet with Bt corn converted feed more efficiently (2.98 vs. 3.38; P = 0.04). Significant differences in ADFI were observed between gender in all three phases, with barrows consuming more feed than gilts (P = 0.0001, 0.003, 0.0003 for phase 1, 2, and 3, respectively). Overall feed consumption of barrows was 24% more than that of gilts.

Table 5. Effects of corn source and sex on growth performance of growing-finishing swine during three feeding phases.

Item[a]	Dietary treatments[b,c]					*P*-values		
	C-G	C-B	Bt-G	Bt-B	SEM	Treatment	Sex	Treatment × sex
Phase 1 (60 to 80 kg)								
ADG (kg)	0.754	0.890	0.658	0.707	0.045	0.01	0.07	0.36
ADFI (kg)	2.16	2.62	2.14	2.61	0.14	0.81	0.0001	0.93
FCR (feed:gain)	2.89	2.98	3.32	3.74	0.18	0.01	0.19	0.36
Phase 2 (81 to 90 kg)								
ADG (kg)	0.755	0.737	0.827	0.933	0.062	0.06	0.50	0.35
ADFI (kg)	2.29	2.68	2.33	2.75	0.22	0.60	0.003	0.87
FCR (feed:gain)	3.09	3.66	2.98	2.97	0.16	0.04	0.13	0.12
Phase 3 (91 to 110+ kg)								
ADG (kg)	0.857	0.991	0.818	1.03	0.068	0.98	0.06	0.61
ADFI (kg)	2.71	3.60	2.58	3.67	0.19	0.77	0.0003	0.32
FCR (feed:gain)	3.18	3.64	3.19	3.57	0.18	0.89	0.07	0.83
Overall (60 to 110+ kg)								
Initial weight (kg)	58.71	63.05	59.45	63.42	2.74	0.53	<.0001	0.83
Final weight (kg)	92.84	100.02	92.19	99.54	1.82	0.75	0.0002	0.96
ADG (kg)	0.733	0.828	0.718	0.803	0.032	0.52	0.006	0.88
ADFI (kg)	2.28	2.78	2.31	2.78	0.15	0.91	0.0001	0.97
FCR (feed:gain)	3.11	3.35	3.22	3.46	0.04	0.003	<.0001	0.97

[a]ADFI: average daily feed intake; ADG: average daily gain; FCR: feed conversion ratio

[b]C and Bt indicate corn source (control and biotechnology-derived); G and B indicate gilts and barrows, respectively.

[c]4 pigs per pen; 16 pigs per treatment

There was a difference (P = 0.0005; Table 6) in ADFI between pigs slaughtered at 85 kg (A) and 100 kg (B). Pigs in group B consumed 390 g/day more feed compared to those in group A. This translated into a greater ADG for pigs in group B (P = 0.0016). Pigs slaughtered at 85 kg gained 105 g/day less than those harvested at 100 kg. However, FCR was not different between pigs within the two slaughter groups (A: 3.26 vs. B: 3.32; P = 0.07). There were no market weight × treatment interactions observed in any of the parameters. Significant market weight × gender interactions were observed for slaughter weight (P = 0.002), ADFI (P = 0.02), ADG (P = 0.01), and FCR (P = 0.003). Barrows in both slaughter groups weighed heavier than gilts. Likewise, barrows in both slaughter groups had greater ADFI, ADG and FCR than gilts.

Table 6. Effects of slaughter weight in growing-finishing swine.

Parameter[a]	Slaughter weights[b]		*P*-values			
	A	B	Slaughter weight	Slaughter weight × treatment	Slaughter weight × gender	SEM
Number of pens[c]	8	8	-	-	-	-
Slaughter weight (kg)	84.41	107.88	<.0001	0.52	0.002	1.28
ADFI (kg)	2.33	2.72	0.0005	0.57	0.020	0.05
ADG (kg)	0.718	0.823	0.0016	0.33	0.010	0.022
FCR (feed:gain)	3.26	3.32	0.0700	0.05	0.001	0.02

[a]ADFI: average daily feed intake; ADG: average daily gain; FCR: feed conversion ratio.
[b]Average slaughter weight: A= 85 kg; B= 100 kg.
[c]4 pigs per pen; 16 pigs per treatment

Carcass Characteristics

Corn effects. No differences were observed between carcass characteristics obtained from pigs fed Bt corn and pigs fed control corn (Table 7). Pigs fed control corn and Bt corn had carcass yields of 72.43 % ± 0.45 and 71.29% ± 0.45, respectively. Calculated percentage lean (NPPC procedure, 2001) was approximately 53% for pigs from both treatment groups. Ultimate carcass temperature for both groups fed control corn and Bt corn was 2.07 °C ±

0.11. Ultimate carcass pH (pH_u) was 5.43 and 5.41 ± 0.02 for control group and Bt group, respectively. No treatment effects were observed for loin eye area (LEA), star probe values (tenderness), percent drip loss, and chemical composition of *longissimus* muscle (Table 8). For the *longissimus* muscle color, significant differences were observed only for the b value. A higher b value denotes greater intensity of yellow color. Results suggest that pigs fed control corn had *longissimus* muscle with greater intensity yellow color compared to pigs fed Bt corn (11.71 vs. 11.31; P = 0.02).

Table 7. Comparison of carcass characteristics of pigs fed Bt corn and control corn (mean values of combined gilts and barrows).

	Corn Line[a]			
Item	Control	Bt	*P*-value	SEM
Number of pens[b]	8	8	-	-
Slaughter weight, kg	96.43	95.86	0.75	1.28
Hot carcass weight, kg	69.97	68.46	0.29	1.00
Carcass yield, %	72.43	71.29	0.06	0.45
Backfat, mm				
1st rib	30.7	30.6	0.92	0.88
10th rib	16.83	17.58	0.52	0.83
Last rib	19.22	17.9	0.78	0.80
Last lumbar vertebrae	16.87	17.06	0.86	0.79
Calculated percent lean[c]	53.60	53.65	0.95	0.64
Loin eye area, cm^2	13.85	14.23	0.51	0.41
Carcass temperature, °C				
1 hour	31.92	31.93	0.96	0.29
6 hours	9.41	9.98	0.18	0.29
24 hours	2.08	2.07	0.97	0.11
Carcass pH				
1 hour	6.00	6.02	0.78	0.05
6 hours	5.56	5.61	0.24	0.03
24 hours	5.43	5.41	0.65	0.02

[a]Control: consists of combined grains from a number of non-genetically modified inbred lines; Bt: Bt 11 (Syngenta Seeds, Inc)

[b]4 pigs per pen; 32 pigs per treatment

[c]Calculation for Percent Lean (National Pork Producers Council, 2001): % Lean = (SFFL/ Hot carcass wt.) x 100, where: Standardized fat free lean, lb (SFFL) = 8.588 + (0.465 x hot carcass wt., lb.) – (21.896 x 10^{th} rib fat depth, in.) + (3.005 x 10^{th} rib loin muscle area, sq. in.)

Table 8. Effects of corn line on *longissimus* muscle quality and composition (mean values of combined gilts and barrows)

Item	Corn Line[a] Control	Bt	*P*-value	SEM
Number of pens[b]	8	8	-	-
Longissimus muscle quality measurements				
Star probe value, kg	5.66	5.47	0.35	0.14
Drip loss, %	6.32	5.54	0.06	0.29
Hunter L value	52.20	51.52	0.39	0.56
Hunter a value	6.79	6.45	0.09	0.14
Hunter b value	11.71	11.31	0.02	0.12
Chemical composition, %				
Protein	22.81	22.74	0.54	0.08
Fat	2.08	2.16	0.78	0.20
Moisture	73.57	73.47	0.51	0.10

[a] Control: consists of combined grains from a number of non-genetically modified inbred lines; Bt: Bt 11 (Syngenta Seeds, Inc)
[b] 4 pigs per pen; 32 pigs per treatment

Gender and slaughter weight effects. Barrows, in general, were 7.25 kg heavier than gilts at slaughter. However, barrows and gilts had an average carcass yield of 71.61% and 72.11%, respectively, which were not statistically different (P = 0.39; Table 9). No difference (P = 0.15) was observed in the first rib backfat between gilts (29.76 mm) and barrows (31.55 mm). However, barrows had thicker 10^{th} rib (20.28 mm vs.14.13 mm; P < 0.0001), last rib (19.48 mm vs. 16.63 mm; P = 0.01), and last lumbar vertebrae (19.52 mm vs. 14.41 mm; P < 0.0001) backfat compared to gilts (Table 9). In addition, barrows had five percentage units less carcass lean compared to gilts (51.03% vs. 56.22%; P < 0.0001). Gilts had significantly larger LEA than barrows. The LEA from gilts were bigger than LEA from barrows by 1.65 cm^2 (14.87 cm^2 vs. 13.22 cm^2; P = 0.006). As expected, pigs slaughtered at a 100 kg weight had larger LEA compared to those harvested at 85 kg. The LEA from heavier pigs was larger by 3.27 cm^2 (15.68 cm^2 vs. 12.41 cm^2; P < 0.0001).

The average ultimate temperature of carcasses from gilts was 1.48 °C which was 1.2 °C lower than that of barrow carcasses (P < 0.0001; Figure 3). Barrow carcasses, both from

control and Bt treatments, were warmer compared to those of the gilts. It can be noted that barrow carcasses, both from the control and Bt treatments, had numerically higher pH at 1 h post-slaughter compared to gilt carcasses. However, the extent of pH decline of barrow carcasses appeared to be greater compared to the gilt carcasses (Figure 4). Average pH_u of barrow carcasses was 5.35 and was significantly lower compared to pH_u of gilt carcasses which was 5.49 (P = 0.0001; Figure 4).

Table 9. Effects of gender and slaughter weight on carcass characteristics.

	Gender			Slaughter weight[a]			
Item	Gilt	Barrow	*P*-value	A	B	*P*-value	SEM
Number of pens[b]	8	8	-	8	8	-	-
Slaughter weight, kg	92.52	99.77	0.0002	84.41	107.88	<.0001	1.28
Hot carcass weight, kg	66.74	71.69	0.001	59.87	78.56	<.0001	1.00
Carcass yield, %	72.11	71.61	0.39	70.89	72.83	0.0019	0.43
Backfat, mm							
1st rib	29.76	31.55	0.15	29.56	31.75	0.08	0.88
10th rib	14.13	20.28	<.0001	15.12	19.29	0.0008	0.83
Last rib	16.63	19.48	0.01	16.35	19.76	0.004	0.80
Last lumbar vertebrae	14.41	19.52	<.0001	14.92	19.01	0.0006	0.79
Calculated percent lean[c]	56.22	51.03	<.0001	54.38	52.87	0.10	0.64
Loin eye area, cm^2	14.87	13.22	0.006	12.41	15.68	<.0001	0.41
Carcass temperature, °C							
1 hour	30.86	32.99	<.0001	31.31	32.54	0.004	0.29
6 hours	8.98	10.41	0.0012	7.87	11.52	<.0001	0.29
24 hours	1.48	2.68	<.0001	3.14	1.02	<.0001	0.11
Carcass pH							
1 hour	5.96	6.07	0.14	6.00	6.02	0.78	0.05
6 hours	5.57	5.60	0.47	5.57	5.61	0.40	0.03
24 hours	5.49	5.35	0.0001	5.37	5.46	0.02	0.02

[a]A: 85 kg; B: 100 kg.

[b]4 pigs per pen; 32 gilts, 32 barrows; 32 pigs in each slaughter weight.

[c]Calculation for Percent Lean (National Pork Producers Council, 2001): % Lean = (SFFL/ Hot carcass wt.) x 100, where: Standardized fat free lean, lb (SFFL) = 8.588 + (0.465 x hot carcass wt., lb.) – (21.896 x 10^{th} rib fat depth, in.) + (3.005 x 10^{th} rib loin muscle area, sq. in.)

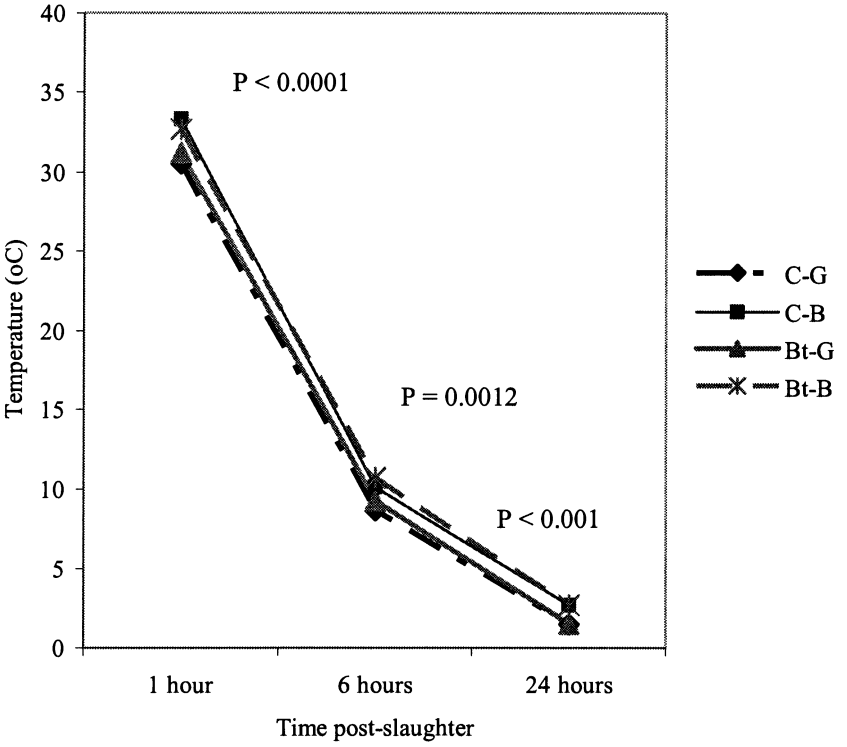

Figure 3. Drop in temperature of carcasses from each dietary treatment.

Dietary treatments: C-G (Control–Gilt); C-B (Control-Barrow); Bt-G (Bt-Gilt); Bt-B (Bt-Barrow)
Standard errors: 1 hour (0.41); 6 hour (0.42); 24 hours (0.16)

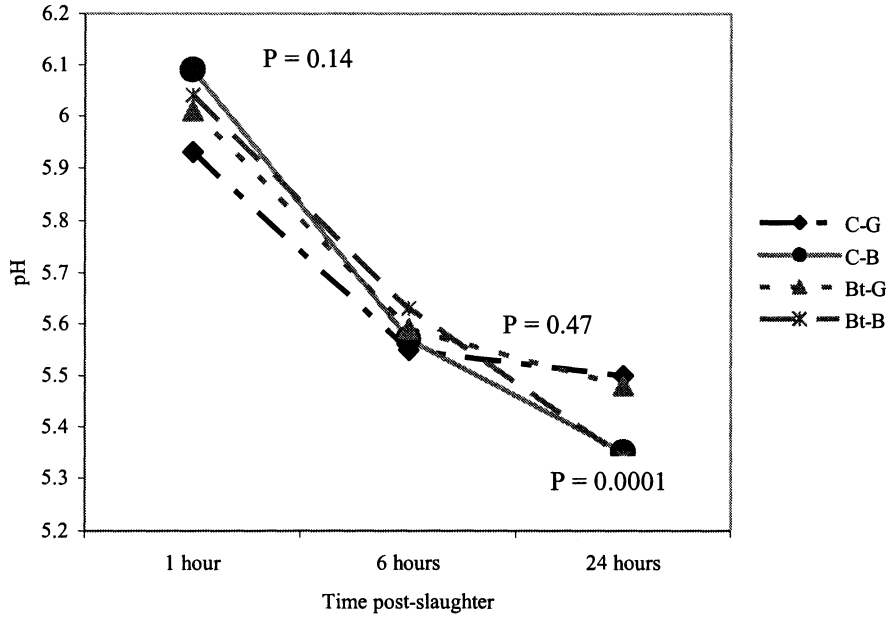

Figure 4. Drop in pH of carcasses from each dietary treatment.

Dietary treatments: C-G (Control–Gilt); C-B (Control-Barrow); Bt-G (Bt-Gilt); Bt-B (Bt-Barrow).
Standard errors: 1 hour (0.06); 6 hour (0.04); 24 hours (0.04).
Slope of line: C-G (-0.215); C-B (-0.37); Bt-G (-0.265); Bt-B (-0.35)

Pigs harvested at 100 kg had approximately two percentage units greater carcass yield, compared to those harvested at 85 kg (P = 0.0019; Table 9). There were no differences observed for 1st rib backfat between the two slaughter weights. However, pigs harvested at 100 kg had significantly thicker 10th rib (19.29 mm vs. 15.12 mm), last rib (19.76 mm vs. 16.35 mm) and last lumbar vertebrae backfat (19.01 mm vs. 14.92 mm). Calculated percentage lean was numerically less in pigs slaughtered at a 100 kg but was not statistically less (52.87% vs. 54.38%; P = 0.10). The average ultimate temperature of carcasses from pigs harvested at 85 kg was 2.12 °C lower than that of carcasses from 85 kg pigs. Average pH_u of carcasses from pigs harvested at a 85 kg was 5.37, which was significantly less than carcass pH from harvested at 100 kg (5.46; P = 0.02).

Table 10 shows the effect of gender and slaughter weights on the quality of the *longissimus* muscle. No differences between gender were observed for *longissimus* muscle tenderness and percentage drip loss. For the *longissimus* muscle color, no differences were observed for 'L' and 'a' values. However, the 'b' value for *longissimus* muscle obtained from gilt carcasses was greater (11.79 vs. 11.23; $P = 0.002$). No gender effects were observed for protein, fat, and moisture content of the samples.

No slaughter weight effects were observed for tenderness and percentage drip loss. Slaughter weight did not affect the 'L' and 'a' color values, however, 'b' value was greater for 85 kg pigs (11.76 vs. 11.26; $P = 0.005$). No effect of slaughter weight was observed for protein, fat, and moisture content of the *longissimus* muscle samples.

No corn line × gender, and corn line × slaughter weight interactions were observed for any of the meat quality parameters measured. Slaughter weight × gender interactions were observed for LEA ($P = 0.002$) and ultimate temperature ($P < 0.0001$). Gilts harvested at 85 kg and barrows harvested at 100 kg had larger LEA (14.16 cm^2 vs. 10.65 $cm^2 \pm 0.57$ and 15.78 cm^2 vs. 15.57 $cm^2 \pm 0.57$, respectively). Barrow carcasses from the 85 kg group had lower carcass ultimate temperature (2.51 °C vs. 3.78 °C ± 0.16). On the other hand, gilt carcasses from the 100 kg group had lower carcass ultimate temperature (-0.81 °C vs. 2.85 °C ± 0.16).

Table 10. Effects of gender and slaughter weight on quality and chemical composition *longissimus* muscle from growing-finishing pigs fed Bt and control corn.

	Gender			Slaughter weight[a]			
Item	Gilt	Barrow	P-value	A	B	P-value	SEM
Number of pens[b]	8	8	-	8	8	-	-
Longissimus muscle quality measurements							
Star probe value, kg	5.71	5.42	0.16	5.75	5.39	0.08	0.14
Drip loss, %	5.93	5.93	0.99	6.01	5.84	0.67	0.29
Hunter L value	51.78	51.93	0.84	51.45	52.27	0.29	0.55
Hunter a value	6.76	6.48	0.15	6.81	6.43	0.06	0.14
Hunter b value	11.79	11.23	0.002	11.76	11.26	0.005	0.12
Chemical composition, %							
Protein	22.84	22.70	0.24	22.75	22.80	0.70	0.08
Fat	2.01	2.23	0.42	2.08	2.16	0.77	0.20
Moisture	73.56	73.49	0.63	73.57	73.48	0.57	0.11

[a]A: 85 kg; B: 100 kg.
[b] 4 pigs per pen; 32 gilts, 32 barrows; 32 pigs in each slaughter weight

Excretion Characteristics

The excretion data, which were pooled from five collection dates, is presented in Table 11. The amount of feces excreted (g/d/pen) was greater for barrows than gilts (1063 g vs. 1333 g; $P < 0.0001$), but was not different between pigs fed Bt and control corn ($P = 0.05$). Intake of N (g/d/pen) was significantly greater in pigs fed control corn (196 g vs. 182 g; $P = 0.0004$) and in barrows (198 g vs. 180 g; $P < .0001$). However, there were treatment × gender interactions observed for N intake ($P = 0.02$), which may have been influenced by the much greater intake of barrows fed the control corn. Amount of N in feces did not differ in pigs fed Bt and control corn (36.1 g vs. 36.5 g ± 1.38; $P = 0.75$). Barrows, however, excreted an average of 8 g more N in feces compared to gilts (40 g vs. 32 g ± 1.38; $P < 0.0001$). There were no interactions observed for N in feces between treatment groups. Percentage N in urine did not differ between pigs fed Bt and control corn ($P = 0.28$), but was significantly greater in gilts than barrows (1.1% vs. 0.9%; $P = 0.0082$). Phosphorus intake (g/d/pen) was also greater in pigs fed control corn (69 g vs. 46 g; $P < 0.0001$) and in barrows (68 g vs. 47 g). There was

an interaction between treatment and gender for P intake ($P < 0.0001$), which may have been influenced by the greater P intake in barrows fed the control corn. Amount of P in feces (g/d/pen) did not differ between pigs fed Bt and control corn (26.14 g vs. 26.48 g; $P = 0.69$), but was significantly greater in barrows compared to gilts (28 g vs. 24 g; $P < 0.0001$). There were no interactions observed for fecal P between treatment groups.

Apparent digestibility of N was 1.4 percentage units greater in pigs fed control corn than those fed with Bt corn (80.9% vs. 79.5%; $P = 0.04$), and 2.9 percentage units greater in gilts compared to barrows (81.7% vs. 78.8% $P = 0.0001$). On the other hand, apparent digestibility of P was 17.6 percentage units greater in pigs fed control corn (57.8% vs. 40.2%; $P < 0.0001$), but was 8.5 percentage units greater in barrows compared to gilts (53.28% vs. 44.72%; $P = 0.0028$). Treatment × gender interactions ($P = 0.0315$) were observed for apparent digestibility of N, with barrows fed Bt corn and gilts fed control corn having lower percent apparent N digestibility (77.27% vs. 80.29% and 81.61% vs. 81.72%, respectively). Treatment × gender interactions ($P = < 0.0001$) were also observed for apparent digestibility of P, with barrows fed control corn and gilts fed Bt corn having greater percent apparent P digestibility (68.28% vs. 47.38 % and 42.07% vs. 38.29%, respectively).

Table 11. Least square means of N and P in feces and urine from pigs fed Bt (B) and control diets (C).[a]

Item	Treatments[b]				SEM	P-value for		
	C-G	C-B	Bt-G	Bt-B		Treatment	Sex	Treatment × Sex
Feed intake (DM), g/day/pen	8298.86	10385.52	8481.88	10195.86	188.39	0.9858	<0.0001	0.3200
Feces excreted (DM), g/day/pen	1034.99	1281.90	1090.56	1384.69	40.74	0.0534	<0.0001	0.5590
Nitrogen								
N intake, g/d/pen	183.17	209.78	178.07	185.91	3.92	0.0004	<0.0001	0.0183
Fecal N, g/d/pen	32.96	40.09	31.78	40.41	1.38	0.7538	<0.0001	0.5854
Urinary N, %	1.12	0.96	1.08	0.84	0.08	0.2852	0.0082	0.5705
Apparent digestibility of N, %	81.61	80.29	81.72	77.27	0.72	0.0455	0.0001	0.0315
Phosphorus								
P intake, g/d/pen	50.23	88.75	44.63	47.07	3.23	<0.0001	<0.0001	<0.0001
Fecal P, g/d/pen	24.68	28.29	23.75	28.52	0.93	0.6988	<0.0001	0.5247
Apparent digestibility of P, %	47.38	68.28	42.07	38.29	2.78	<0.0001	0.0028	<0.0001

[a] Pooled data from 5 collection dates.

[b] 4 pens per treatment; 4 pigs per pen; C and Bt indicate corn source (control and biotechnology-derived); G and B indicate gilts and barrows, respectively.

CHAPTER 5. DISCUSSION

Corn effects

Results of the experiment showed that corn type had no effect on feed intake and average daily gain. This is consistent with other feeding trials which compared genetically modified corn and conventional corn varieties (Weber et al., 2000; Reuter et al., 2001; Stanisiewski et al., 2001; Fischer et al., 2002; Bressner et al., 2002). In contrast, Piva et al. (2001) found that average daily gain was greater in pigs fed Bt corn (MON 810), and the difference was attributed to lower fumonisin B_1 concentrations in Bt corn grains. In the current experiment, pigs fed diets with control corn had greater feed efficiency than pigs fed diets with Bt corn. However, the control corn consisted of a mixture of grains from non-genetically inbred corn lines and does not represent the exact isogenic counterpart of the Bt 11 variety. Hence, no direct relationship between the presence of the Bt gene and the reduced feed efficiency can be made. In addition, analysis of the growth performance by feeding phase showed that the difference in FCR was not consistent from phases 1 to 3. Thus, this difference could have been more of a function of better performance of some pigs in the control group rather than due to the negative effect of the Bt corn on feed efficiency.

The type of corn in the diet did not affect the carcass weight and carcass yield in the current experiment. This was consistent with the experiment reported by Fischer et al. (2002), Bressner et al. (2002), and Hyun et al. (2004), and was in contrast with Weber et al. (2000), in which pigs fed conventional corn were heavier during slaughter and had greater dressing percentages. Piva et al. (2001), on the other hand, found that pigs fed Bt corn were 2.8% heavier at slaughter. In agreement with most studies mentioned, no corn effects were observed for backfat thickness. Weber et al. (2000), however, found that pigs fed isogenic

control corn had greater backfat depth at 10^{th} rib and last lumbar vertebrae. No corn effects were observed for LEA, star probe and drip loss, which agreed with the studies mentioned above. In the current study, Hunter color 'b' value was found to be significantly greater in pigs fed control corn and was in contrast with results reported by Hyun et al. (2004), wherein no differences were observed for Minolta b* value. Results of the analysis of the longissimus muscle for protein, fat, and moisture content did not reveal any effect of corn variety, and agrees with findings reported by Fischer et al. (2002) and Hyun et al. (2004).

Although other feeding trials involved feeding of genetically modified corn in pigs, none of the studies reviewed used Bt "Event 11". A study in broilers involving Bt 11, however, showed that body weight, feed efficiency, and carcass measures such as dressing %, fat pad %, drums %, thighs %, wings %, and size of pectoralis muscle were not affected by corn source (Brake et al., 2003).

The presence of the Bt gene did not affect the amount of N and P excreted in feces. At present, published data is not available for N and P excretion comparing Bt corn and control corns. Apparent digestibility of N and P were lower in pigs fed Bt corn than those fed control corn. This result may have been confounded by the notably greater N and P intake of barrows in the group fed control corn. Increase in feed intake may not necessarily lead to increase in apparent digestibility of a nutrient. However, studies have demonstrated that increasing feed intake in pigs can result in an increase of endogenous losses of amino acids (Butts et al., 1993, as cited by Gabert et al., 2001). Feed intake was determined by measuring daily feed offering and weekly feed disappearance. However, it is difficult to estimate actual feed consumed by the animals, especially in pen groupings. It is possible that feed wastage could have greatly influenced the results obtained. In general, the apparent N and P

digestibility values obtained were quite high, but still within the range of some studies reported (Kornegay and Harper, 1997; Spencer et al., 2000; Sands et al., 2001).

Variations in results in the current study and other studies involving Bt corn mentioned above, suggest no consistent negative influence of Bt corn on pigs.

Gender effects

Barrows had greater ADFI and ADG, but had greater backfat depth and poorer FCR, which is consistent with the findings of other studies (Weber et al., 2000; Reuter et al., 2001; Fischer et al., 2002; Bressner et al., 2002; Hyun et al., 2004). Gilts had a larger LEA compared to barrows, which agrees with the results of Cromwell et al. (1993) and Weber et al. (2002). Other studies, however, found no differences in LEA between gilts and barrows (Hyun et al., 2004; Bressner et al., 20002). The current study found differences in the ultimate pH of gilt and barrow carcasses, although the average for both sexes (barrows: 5.35; gilts: 5.49) was less than the recommended pH of 5.6 to 5.9 proposed by the National Pork Producers Council (National Pork Board, 1998). This finding contradicts previously published results indicating that gender had no impact on muscle pH (Cisneros et al., 1996; Leach et al., 1996). However, Latorre et al. (2004) found higher ultimate pH in barrows. Factors that influence pH of carcasses include conditions imposed during transportation and holding at the slaughterhouse, and barrows and gilts might respond to the stress differently. In addition, the difference in pH could be related to the difference in the carcass temperature between barrows and gilts, with barrows having warmer carcasses. This was possibly due to the thicker backfat layer in barrow carcasses, which have more likely resulted in slower cooling rates. Decline in pH is due to the conversion of glycogen in the cells to lactic acid. This conversion is accelerated by higher temperature, thus, more lactic acid accumulated in

the barrow carcasses. The difference in pH between gilts and barrows may also explain why the Hunter b value is lower in loin chops of barrows, as lower pH can affect meat color (Hedrick et al, 2003). Another possible explanation for the difference in pH between barrow and gilt carcasses is the difference in the amount of glycogen in their tissues. It is possible that barrows had more stored glycogen in their tissues before slaughter, thus, providing more substrate for lactic acid production.

The amount of feces excreted by barrows was greater than those excreted by gilts, and this may be due to the relatively greater feed consumption of barrows. Because of this, it followed that barrows had greater amount of N and P in their feces. Better feed efficiency in gilts could also explain this observation. Improvement in feed efficiency has been shown to reduce nutrient excretion (van Heughten and van Kempen, 2004). Apparent digestibility of N was greater in gilts than barrows and this may be because gilts were more efficient converters of feed, as reflected by their lower feed conversion ratio. Nitrogen excreted in urine was also greater in gilts compared to barrows. This further supports the observation that gilts were more efficient in utilizing feed because greater percentage N in urine would mean that more feed was absorbed. Thus, excess N in the body was excreted via the urinary system as opposed to being excreted via feces when nutrients are not absorbed in the gut. Apparent digestibility of P was, on the other hand, greater in barrows. As explained above, the much greater feed consumption in barrows in the control group, could have confounded the result. In addition, the result was inconsistent because there was gender × treatment interaction observed, with barrows in the Bt group having lesser apparent P digestibility compared to gilts in the same group (38.29% vs. 42.07%), and barrows in the control group having greater apparent P digestibility than gilts in the control group (68.28% vs. 47.38%).

Slaughter weight effects

Pigs slaughtered at 100 kg had greater ADFI which is in contrast with the results published by Latorre et al. (2004), wherein slaughter weight did not influence ADFI. However, Cisneros et al. (1996) reported that ADFI increased 100 g/d for every 10 kg increase in body weight. The increase in ADG with the increase in slaughter weight agrees with the results of Cisneros et al. (1996) and Johnston et al. (1993). Other published results, however, indicated that ADG decreased with increasing slaughter weights (Latorre et al, 2004). Differences in the results could be due to differences of breeds used by different investigators. For example, Latorre et al. (2004) worked with Pietrain which is an early-maturing breed whose ADG declines rapidly at body weight in excess of 100 kg.

In agreement with Latorre et al. (2004), but in contrast with Cisneros et al. (1996) and Fortin (1980), greater carcass percentage yield was observed from heavier pigs in the current experiment. However, even though this was the case, carcass percentage lean did not differ significantly between 85 kg and 100 kg pigs. This was because the 100 kg pigs have significantly greater 1^{st}, 10^{th}, last rib and last lumbar vertebrae fat depth, thus, had more fat than 85 kg pigs. Increase in backfat with increased weight was also reported by Cisneros et al. (1996). Slaughter weight has been found to have no effect on carcass pH in most studies (Garcia-Macias et al., 1996; Leach et al., 1996). In our study, the difference in ultimate pH could again be attributed to the temperature differences of the light and heavy carcasses. Consistent with the explanation provided for the difference in pH in barrows and gilts, there could have been greater metabolism of glycogen in the light carcasses which resulted in more lactic acid production. The average 24 h temperature of carcasses from pigs in the 85 kg group was higher (3.14 °C) compared to carcasses from the 100 kg group (1.02 °C). This was

possibly due to the thicker backfat layer in pigs slaughtered at 100 kg, which have more likely resulted in slower cooling rates.

Analyzing data with slaughter date as a covariate, it was found that carcass temperature was different at all time points (1 h, 6 h, and 24 h; $P < 0.0001$ for all time points; Appendix 1) during the four slaughter dates. Ultimate pH (24 h) was also affected by slaughter date ($P < 0.0001$). These observations further support the explanation of the differences in carcass temperature and pH_u, because average carcass temperature was greater, and average pH_u was less, during those days when barrows were slaughtered. There were differences in the average time between exsanguination and chilling of carcasses between four slaughter dates, however, these were not statistically significant (Appendix 1). Environmental temperature and humidity during transport of the pigs from the farm to the slaughter facility were included as covariates, as these factors can affect the stress level of the animals, hence, affecting meat quality. Weather data during the hauling days was obtained from National Climatic Data Center database. Differences in the environmental temperature during the four hauling days were not statistically significant (Appendix 2). However, relative humidity was greater during those days when gilts were hauled. It is possible that this could have caused more stress on the gilts than barrows, causing more glycogen in gilts to be depleted prior to slaughter. Hence, gilt carcasses had higher carcass ultimate pH than barrows.

CHAPTER 6. CONCLUSION

This study demonstrated that Bt 11 corn (containing the *cry 1Ab* gene and the *pat* gene) can be fed to growing-finishing pigs without significant differences on feed consumption, daily weight gain, and nutrient excretion. Carcass and meat quality parameters were not negatively affected by Bt 11 corn. The results suggest that feeding Bt 11 corn in pigs provides no advantages or disadvantages over conventional corn varieties used as feedstuff for swine. This study confirms the result of previous studies involving other genetically modified corn varieties, and hence, it can be concluded that Bt 11 corn is substantially equivalent to conventional corn varieties in terms of feeding value in swine.

APPENDIX

Appendix 1. Average carcass temperature, pH, and time interval between exsanguination and chilling of carcasses during the four slaughter dates.

Slaughter date	Animal profile (gender, ave. weight)	Temperature (°C)			pH			Time interval (minutes)
		1 h	6 h	24 h	1 h	6 h	24 h	
1	Barrow, 85 kg	31.78	7.42	2.51	6.01	5.60	5.24	47.37
2	Gilt, 85 kg	30.82	8.31	3.78	6.00	5.54	5.51	42.75
3	Barrow, 100 kg	34.18	13.38	2.85	6.12	5.60	5.45	40.06
4	Gilt, 100 kg	30.90	9.65	-0.81	5.93	5.60	5.47	48.62
SEM		0.41	0.42	0.16	0.06	0.04	0.04	1.24
P-value		<0.0001	<0.0001	<0.0001	0.29	0.57	<0.0001	0.87

Appendix 2. Environmental temperature and relative humidity during the four hauling dates.

Hauling date	Animal profile (gender, ave. weight)	Temperature (°C)	Relative humidity (%)
1	Barrow, 85 kg	23	20
2	Gilt, 85 kg	28	27
3	Barrow, 100 kg	31	27
4	Gilt, 100 kg	20	55
SEM		2.46	7.76
P-value		0.315	<0.0001

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